

Lab 07: Comparing phylogenetic hypotheses

I. Open MacClade

A. If MacClade is *not* on the hard drive

1. Log onto the Macintosh Software server (Apple Menu -> Chooser -> Apple Share -> Network backbone -> College Server)
2. Open the Biology folder, and find the MacClade folder
3. Drop the MacClade folder into the hard drive
4. Close and discard the server

B. If MacClade is on the hard drive

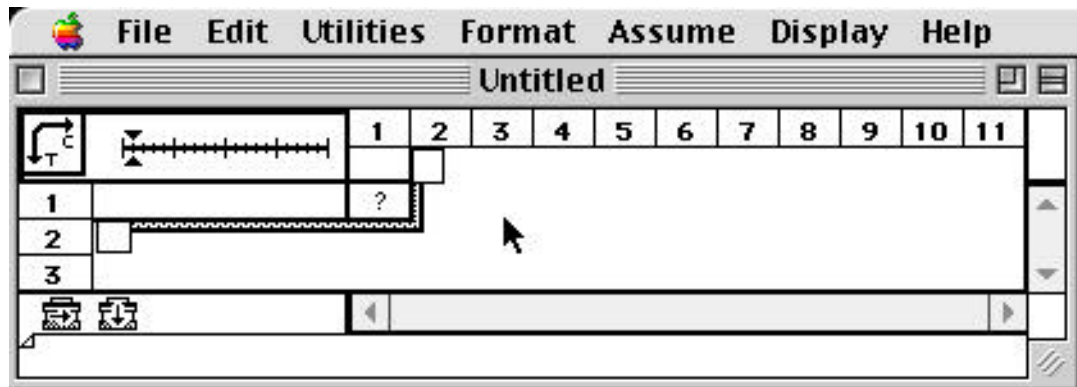
1. Open the MacClade folder on the hard drive and double click on the MacClade icon
2. In the open file window, select "New"



MacClade 3.07 §

II. Assemble your data

A. The first window you see when you open MacClade is the Data Editor window. It displays a 1x1 spreadsheet. Each column will be used to list characters, and each row will be used to list taxa (in your case, the taxa are species).



1. Add rows and columns using the Add option in the Utilities menu.
2. In the leftmost cell of each row, put the name of the taxon
3. In the topmost cell of each column, put the name of the characters you measured.
4. Fill the cells with your categorical measurements from page 2 of last week's lab.

B. Save the Data editor file onto the desktop (in the Guest folder).

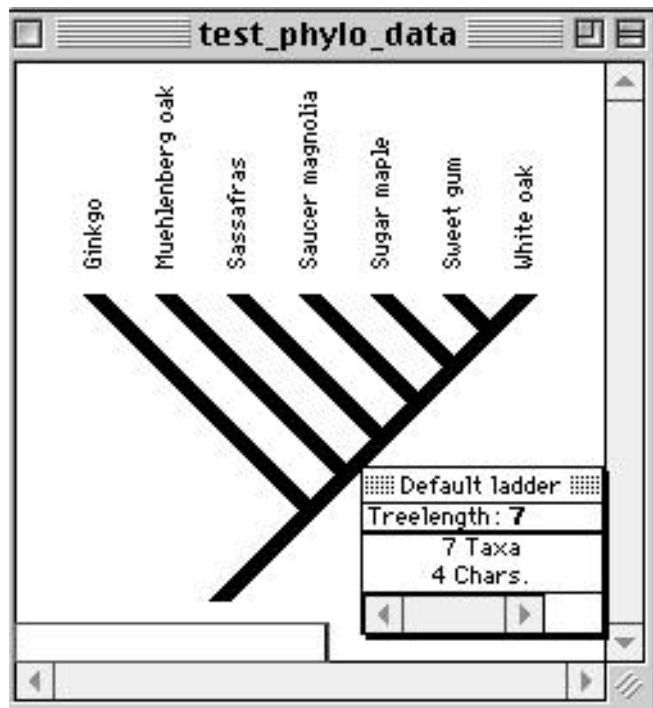
III. Build a phylogeny

A. Generate a phylogeny

1. Select "Go to Tree Window" from the Display menu
2. If no phylogeny file exists, the program will ask what kind of phylogeny you want. Select the "Default Ladder" phylogeny. What appears is a phylogenetic tree that includes all the taxa that are in your editor file. They are in the order that you entered the taxon data.

B. Study this phylogeny

1. There are three windows associated with the phylogeny
 - a. In the main window is the phylogeny: an hypothesis about the organization of your taxa
 - b. The tree legend is in the bottom corner. It summarizes how many taxa and how many characters are associated with this phylogeny. It also identifies the *treelength*, the number of character changes required to hold this



topology. (Treelength will be explained at greater length below.)

- c. The character legend is also in the bottom corner (if it is not, you can make it appear by selecting "Trace Character" from the Trace menu. Turn Trace off for now.)
2. The branches on the phylogeny are movable.
 - a. Select a branch; drag it to another branch. This changes the topology of the phylogeny.
 - b. Note that changing the branch positions can change the treelength.
3. You can view the evolution of your measured characters by scrolling through the Character legend. Look at the changes that must occur in order for the phylogeny to exist in its given topology.

C. Store this phylogeny

1. In the Tree menu, select "Store tree"
2. Give the phylogeny a name, such as "default ladder"
3. Later, When you reopen your file, this phylogeny will be in the file.

IV. Generating alternative hypotheses

The treelength is an index of how many evolutionary events occurred in a given phylogeny. An evolutionary event is counted every time a change occurred from one character state to another. MacClade allows you to see the evolutionary changes in each of your phylogenies by coloring the branches. A change in color means a change in character state.

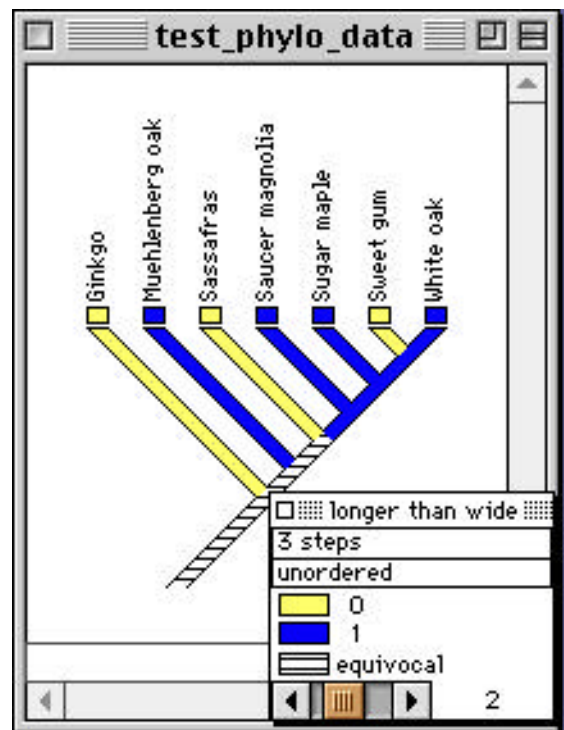
For example, look at your default phylogeny. Turn the Trace Character option on again. You will see some branches in blue, and some in yellow. In the character legend is the name of the traced character, (here it's "longer than wide") and an indication of which color corresponds to which character state. Here yellow corresponds to "0" which I define as not longer than wide, and blue corresponds to "1" which I define as longer than wide. The hatched branches could be either blue or yellow: there aren't enough data for the computer to resolve which they should be. At the bottom of the character legend is a scroll bar that allows you to view the changes in other characters.

In this window, we see three evolutionary steps:
(if we assume that the ancestor was in a 0 state)

- 1) from a 0 state to a 1 state in the Muehlenberg oak lineage
- 2) from the same 0 state to a 1 state in the lineage that leads to the four right species, and
- 3) from a 1 back to a 0 state in the Sweet gum lineage.

Since we don't know the ancestral state, it is equally plausible that it was in the "1" state, and that the three steps were:

- 1) from 1 to 0 in the Ginkgo species
- 2) from the same 1 to 0 in the Sassafras species, and
- 3) from the same 1 to 0 in the Sweet gum lineage.



In other words, the computer takes a phylogeny, then maps all the character states on it that you have entered in the data file. It indicates the minimum number of evolutionary events that must have happened in that phylogeny so that each species has the character states that you listed. The total number of steps, summed across all the characters that you included in the data set, is the treelength.

A. Move the phylogeny branches around to see if you can change the treelength.

1. Put your cursor on a branch and click down.
2. Drag your cursor (and the branch) to a new branch.
3. Unclick, and the branch should jump to the new position. Note that the old branch will anchor in a place on the new branch that allows the names across the top to be evenly distributed. This should emphasize to you that the height of a node is not meaningful. The only meaningful thing is the position of a node relative to other nodes above and below it.

B. Generate 50 random phylogenies

1. Select "Go to Tree Window" from the Display menu
2. Select "Random Trees" from the Tree menu
3. Create 50 equiprobable phylogenies

Draw your most parsimonious phylogeny(ies) here. (Make sure that they are indeed different.) Indicate, with tick marks, what evolutionary events happened, and when (use the method illustrated in figure 2 from last lab). If you are left with only one phylogeny, draw the next most parsimonious phylogeny too.

What are the substantive evolutionary differences in the phylogenies above?

How would you go about determining which phylogeny was a more likely representation of the true relationships among the organisms?